

# RAW SEQUENCE LISTING

EFS

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/567,894A

Source: IFWD

Date Processed by STIC: 2/7/07

# **ENTERED**



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/567,894A

DATE: 02/07/2007

TIME: 11:41:57

Input Set : N:\efs\02\_07\_07\10567894a\_efs\FBRIC54SeqList.txt  
 Output Set: N:\CRF4\02072007\J567894A.raw

3 <110> APPLICANT: James, David  
 4 Govers, Roland  
 6 <120> TITLE OF INVENTION: Novel Translocation Assay  
 8 <130> FILE REFERENCE: FBRIC54.001APC  
 10 <140> CURRENT APPLICATION NUMBER: US 10/567,894A  
 C--> 11 <141> CURRENT FILING DATE: 2006-02-08  
 13 <150> PRIOR APPLICATION NUMBER: AU2003904237  
 14 <151> PRIOR FILING DATE: 2003-08-08  
 16 <150> PRIOR APPLICATION NUMBER: PCT/AU2004/001057  
 17 <151> PRIOR FILING DATE: 2004-08-09  
 19 <160> NUMBER OF SEQ ID NOS: 64  
 21 <170> SOFTWARE: PatentIn version 3.3  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 2128  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Homo sapiens  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (146)..(1672)  
 33 <400> SEQUENCE: 1  
 34 ggggtccca tcggccccgc cctcgacgt cactccggga ccccccggc ctccgcaggt 60  
 36 tctgcgtcc aggccggagt cagagactcc aggatcggtt ctttcatttt cgccggccct 120  
 38 gcgcgtccag ctcttctaag acgag atg ccg tgc ggc ttc caa cag ata ggc 172  
 39 Met Pro Ser Gly Phe Gln Gln Ile Gly  
 40 1 5  
 42 tcc gaa gat ggg gaa ccc cct cag cag cga gtg act ggg acc ctg gtc 220  
 43 Ser Glu Asp Gly Glu Pro Pro Gln Gln Arg Val Thr Gly Thr Leu Val  
 44 10 15 20 25  
 46 ctt gct gtg ttc tct gcg gtg ctt ggc tcc ctg cag ttt ggg tac aac 268  
 47 Leu Ala Val Phe Ser Ala Val Leu Gly Ser Leu Gln Phe Gly Tyr Asn  
 48 30 35 40  
 50 att ggg gtc atc aat gcc cct cag aag gtg att gaa cag agc tac aat 316  
 51 Ile Gly Val Ile Asn Ala Pro Gln Lys Val Ile Glu Gln Ser Tyr Asn  
 52 45 50 55  
 54 gag acg tgg ctg ggg agg cag ggg cct gag gga ccc agc tcc atc cct 364  
 55 Glu Thr Trp Leu Gly Arg Gln Gly Pro Glu Gly Pro Ser Ser Ile Pro  
 56 60 65 70  
 58 cca ggc acc ctc acc acc ctc tgg gcc ctc tcc gtg gcc atc ttt tcc 412  
 59 Pro Gly Thr Leu Thr Leu Trp Ala Leu Ser Val Ala Ile Phe Ser  
 60 75 80 85  
 62 gtg ggc ggc atg att tcc tcc ttc ctc att ggt atc atc tct cag tgg 460  
 63 Val Gly Gly Met Ile Ser Ser Phe Leu Ile Gly Ile Ile Ser Gln Trp  
 64 90 95 100 105

*see p. 6*

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66 ctt gga agg aaa agg gcc atg ctg gtc aac aat gtc ctg gcg gtg ctg	508
67 Leu Gly Arg Lys Arg Ala Met Leu Val Asn Asn Val Leu Ala Val Leu	
68               110               115               120	
70 ggg ggc agc ctc atg ggc ctg gcc aac gct gct gcc tcc tat gaa atg	556
71 Gly Gly Ser Leu Met Gly Leu Ala Asn Ala Ala Ser Tyr Glu Met	
72               125               130               135	
74 ctc atc ctt gga cga ttc ctc att ggc gcc tac tca ggg ctg aca tca	604
75 Leu Ile Leu Gly Arg Phe Leu Ile Gly Ala Tyr Ser Gly Leu Thr Ser	
76               140               145               150	
78 ggg ctg gtg ccc atg tac gtg ggg gag att gct ccc act cac ctg cgg	652
79 Gly Leu Val Pro Met Tyr Val Gly Glu Ile Ala Pro Thr His Leu Arg	
80               155               160               165	
82 ggc gcc ctg ggg acg ctc aac caa ctg gcc att gtt atc ggc att ctg	700
83 Gly Ala Leu Gly Thr Leu Asn Gln Leu Ala Ile Val Ile Gly Ile Leu	
84 170               175               180               185	
86 atc gcc cag gtg ctg ggc ttg gag tcc ctc ctg ggc act gcc agc ctg	748
87 Ile Ala Gln Val Leu Gly Leu Glu Ser Leu Leu Gly Thr Ala Ser Leu	
88               190               195               200	
90 tgg cca ctg ctc ctg ggc ctc aca gtg cta cct gcc ctc ctg cag ctg	796
91 Trp Pro Leu Leu Leu Gly Leu Thr Val Leu Pro Ala Leu Leu Gln Leu	
92               205               210               215	
94 gtc ctg ctc ccc ttc tgt ccc gag agc ccc cgc tac ctc tac atc atc	844
95 Val Leu Leu Pro Phe Cys Pro Glu Ser Pro Arg Tyr Leu Tyr Ile Ile	
96               220               225               230	
98 cag aat ctc gag ggg cct gcc aga aag agt ctg aag cgc ctg aca ggc	892
99 Gln Asn Leu Glu Gly Pro Ala Arg Lys Ser Leu Lys Arg Leu Thr Gly	
100               235               240               245	
102 tgg gcc gat gtt tct gga gtg ctg gct gag ctg aag gat gag aag cgg	940
103 Trp Ala Asp Val Ser Gly Val Leu Ala Glu Leu Lys Asp Glu Lys Arg	
104 250               255               260               265	
106 aag ctg gag cgt gag cgg cca ctg tcc ctg ctc cag ctc ctg ggc agc	988
107 Lys Leu Glu Arg Glu Arg Pro Leu Ser Leu Leu Gln Leu Leu Gly Ser	
108               270               275               280	
110 cgt acc cac cgg cag ccc ctg atc att gcg gtc gtg ctg cag ctg agc	1036
111 Arg Thr His Arg Gln Pro Leu Ile Ile Ala Val Val Leu Gln Leu Ser	
112               285               290               295	
114 cag cag ctc tct ggc atc aat gct gtt ttc tat tat tcg acc agc atc	1084
115 Gln Gln Leu Ser Gly Ile Asn Ala Val Phe Tyr Tyr Ser Thr Ser Ile	
116               300               305               310	
118 ttc gag aca gca ggg gta ggc cag cct gcc tat gcc acc ata gga gct	1132
119 Phe Glu Thr Ala Gly Val Gly Gln Pro Ala Tyr Ala Thr Ile Gly Ala	
120               315               320               325	
122 ggt gtg gtc aac aca gtc ttc acc ttg gtc tcg gtg ttg ttg gtg gag	1180
123 Gly Val Val Asn Thr Val Phe Thr Leu Val Ser Val Leu Leu Val Glu	
124 330               335               340               345	
126 cgg gcg ggg cgc cgg acg ctc cat ctc ctg ggc ctg gcg ggc atg tgt	1228
127 Arg Ala Gly Arg Arg Thr Leu His Leu Leu Gly Leu Ala Gly Met Cys	
128               350               355               360	
130 ggc tgt gcc atc ctg atg act gtg gct ctg ctc ctg ctg gag cga gtt	1276

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/567,894A**

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**Input Set : N:\efs\02\_07\_07\10567894a\_efs\FBRIC54SeqList.txt**  
**Output Set: N:\CRF4\02072007\J567894A.raw**

131	Gly	Cys	Ala	Ile	Leu	Met	Thr	Val	Ala	Leu	Leu	Leu	Glu	Arg	Val		
132				365				370				375					
134	cca	gcc	atg	agc	tac	gtc	tcc	att	gtg	gcc	atc	ttt	ggc	ttc	gtg	gca	1324
135	Pro	Ala	Met	Ser	Tyr	Val	Ser	Ile	Val	Ala	Ile	Phe	Gly	Phe	Val	Ala	
136				380				385			390						
138	ttt	ttt	gag	att	ggc	cct	ggc	ccc	att	cct	tgg	ttc	atc	gtg	gcc	gag	1372
139	Phe	Phe	Glu	Ile	Gly	Pro	Gly	Pro	Ile	Pro	Trp	Phe	Ile	Val	Ala	Glu	
140				395				400			405						
142	ctc	ttc	agc	cag	gga	ccc	cgc	ccg	gca	gcc	atg	gct	gtg	gct	ggg	ttc	1420
143	Leu	Phe	Ser	Gln	Gly	Pro	Arg	Pro	Ala	Ala	Met	Ala	Val	Ala	Gly	Phe	
144				410				415			420			425			
146	tcc	aac	tgg	acg	agc	aac	ttc	atc	att	ggc	atg	ggt	ttc	cag	tat	gtt	1468
147	Ser	Asn	Trp	Thr	Ser	Asn	Phe	Ile	Ile	Gly	Met	Gly	Phe	Gln	Tyr	Val	
148					430				435			440					
150	gcg	gag	gct	atg	ggg	ccc	tac	gtc	ttc	ctt	cta	ttt	gcg	gtc	ctc	ctg	1516
151	Ala	Glu	Ala	Met	Gly	Pro	Tyr	Val	Phe	Leu	Leu	Phe	Ala	Val	Leu	Leu	
152				445				450			455						
154	ctg	ggc	ttc	atc	ttc	acc	ttc	tta	aga	gta	cct	gaa	act	cga	ggc		1564
155	Leu	Gly	Phe	Ile	Phe	Thr	Phe	Leu	Arg	Val	Pro	Glu	Thr	Arg	Gly		
156				460				465			470						
158	cgg	acg	ttt	gac	cag	atc	tca	gct	gcc	ttc	cac	cgg	aca	ccc	tct	ctt	1612
159	Arg	Thr	Phe	Asp	Gln	Ile	Ser	Ala	Ala	Phe	His	Arg	Thr	Pro	Ser	Leu	
160				475				480			485						
162	tta	gag	cag	gag	gtg	aaa	ccc	agc	aca	gaa	ctt	gag	tat	tta	ggg	cca	1660
163	Leu	Glu	Gln	Glu	Val	Lys	Pro	Ser	Thr	Glu	Leu	Glu	Tyr	Leu	Gly	Pro	
164				490				495			500			505			
166	gat	gag	aac	gac	tgaggggcca	ggcagggggtg	ggagagccag	ctctctctac									1712
167	Asp	Glu	Asn	Asp													
170	ccggccccaga	gacccttcc	tttcctctgc	agcacattaa	ccctctcttc	cctattattt											1772
172	ccgggtggaa	aagaatccct	gcagcctgg	agaattggga	agctggggga	agggtggct											1832
174	gagcacccccc	tcattccct	cgtgtgactc	tcttggatta	tttatgtgtt	gtgtttggc											1892
176	cgtggccatc	agggtggggcc	actctccct	cccttccct	tccccatcc	ccttcctcc											1952
178	ccaccttccc	cagactcagc	tccagaatac	cttcttcgct	gctagagaag	gggatttgg											2012
180	gggaagacag	gtctagactt	tctcagtgg	acaaccaga	gcagagagca	ggacaggaga											2072
182	caagaaatcc	agtttcccac	caccctggac	tcctccac	atctggact	ttcact											2128
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186	<211>	LENGTH:	509														
187	<212>	TYPE:	PRT														
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190	<400>	SEQUENCE:	2														
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193	1				5				10					15			
196	Gln	Gln	Arg	Val	Thr	Gly	Thr	Leu	Val	Leu	Ala	Val	Phe	Ser	Ala	Val	
197					20				25				30				
200	Leu	Gly	Ser	Leu	Gln	Phe	Gly	Tyr	Asn	Ile	Gly	Val	Ile	Asn	Ala	Pro	
201					35				40			45					
204	Gln	Lys	Val	Ile	Glu	Gln	Ser	Tyr	Asn	Glu	Thr	Trp	Leu	Gly	Arg	Gln	
205					50				55			60					
208	Gly	Pro	Glu	Gly	Pro	Ser	Ser	Ile	Pro	Pro	Gly	Thr	Leu	Thr	Leu		

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209	65	70	75	80
212	Trp Ala Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Ser Ser			
213	85	90	95	
216	Phe Leu Ile Gly Ile Ile Ser Gln Trp Leu Gly Arg Lys Arg Ala Met			
217	100	105	110	
220	Leu Val Asn Asn Val Leu Ala Val Leu Gly Gly Ser Leu Met Gly Leu			
221	115	120	125	
224	Ala Asn Ala Ala Ala Ser Tyr Glu Met Leu Ile Leu Gly Arg Phe Leu			
225	130	135	140	
228	Ile Gly Ala Tyr Ser Gly Leu Thr Ser Gly Leu Val Pro Met Tyr Val			
229	145	150	155	160
232	Gly Glu Ile Ala Pro Thr His Leu Arg Gly Ala Leu Gly Thr Leu Asn			
233	165	170	175	
236	Gln Leu Ala Ile Val Ile Gly Ile Leu Ile Ala Gln Val Leu Gly Leu			
237	180	185	190	
240	Glu Ser Leu Leu Gly Thr Ala Ser Leu Trp Pro Leu Leu Leu Gly Leu			
241	195	200	205	
244	Thr Val Leu Pro Ala Leu Leu Gln Leu Val Leu Leu Pro Phe Cys Pro			
245	210	215	220	
248	Glu Ser Pro Arg Tyr Leu Tyr Ile Ile Gln Asn Leu Glu Gly Pro Ala			
249	225	230	235	240
252	Arg Lys Ser Leu Lys Arg Leu Thr Gly Trp Ala Asp Val Ser Gly Val			
253	245	250	255	
256	Leu Ala Glu Leu Lys Asp Glu Lys Arg Lys Leu Glu Arg Glu Arg Pro			
257	260	265	270	
260	Leu Ser Leu Leu Gln Leu Leu Gly Ser Arg Thr His Arg Gln Pro Leu			
261	275	280	285	
264	Ile Ile Ala Val Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn			
265	290	295	300	
268	Ala Val Phe Tyr Tyr Ser Thr Ser Ile Phe Glu Thr Ala Gly Val Gly			
269	305	310	315	320
272	Gln Pro Ala Tyr Ala Thr Ile Gly Ala Gly Val Val Asn Thr Val Phe			
273	325	330	335	
276	Thr Leu Val Ser Val Leu Leu Val Glu Arg Ala Gly Arg Arg Thr Leu			
277	340	345	350	
280	His Leu Leu Gly Leu Ala Gly Met Cys Gly Cys Ala Ile Leu Met Thr			
281	355	360	365	
284	Val Ala Leu Leu Leu Glu Arg Val Pro Ala Met Ser Tyr Val Ser			
285	370	375	380	
288	Ile Val Ala Ile Phe Gly Phe Val Ala Phe Phe Glu Ile Gly Pro Gly			
289	385	390	395	400
292	Pro Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg			
293	405	410	415	
296	Pro Ala Ala Met Ala Val Ala Gly Phe Ser Asn Trp Thr Ser Asn Phe			
297	420	425	430	
300	Ile Ile Gly Met Gly Phe Gln Tyr Val Ala Glu Ala Met Gly Pro Tyr			
301	435	440	445	
304	Val Phe Leu Leu Phe Ala Val Leu Leu Leu Gly Phe Phe Ile Phe Thr			
305	450	455	460	

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308 Phe Leu Arg Val Pro Glu Thr Arg Gly Arg Thr Phe Asp Gln Ile Ser  
309 465 470 475 480  
312 Ala Ala Phe His Arg Thr Pro Ser Leu Leu Glu Gln Glu Val Lys Pro  
313 485 490 495  
316 Ser Thr Glu Leu Glu Tyr Leu Gly Pro Asp Glu Asn Asp  
317 500 505  
320 <210> SEQ ID NO: 3  
321 <211> LENGTH: 1566  
322 <212> TYPE: DNA  
323 <213> ORGANISM: Artificial sequence  
325 <220> FEATURE:  
326 <223> OTHER INFORMATION: Homo sapiens GLUT4 with HA tag  
329 <220> FEATURE:  
330 <221> NAME/KEY: CDS  
331 <222> LOCATION: (1)..(1566)  
333 <400> SEQUENCE: 3  
334 atg ccg tcg ggc ttc caa cag ata ggc tcc gaa gat ggg gaa ccc cct 48  
335 Met Pro Ser Gly Phe Gln Gln Ile Gly Ser Glu Asp Gly Glu Pro Pro  
336 1 5 10 15  
338 cag cag cga gtg act ggg acc ctg gtc ctt gct gtg ttc tct gcg gtg 96  
339 Gln Gln Arg Val Thr Gly Thr Leu Val Leu Ala Val Phe Ser Ala Val  
340 20 25 30  
342 ctt ggc tcc ctg cag ttt ggg tac aac att ggg gtc atc aat gcc cct 144  
343 Leu Gly Ser Leu Gln Phe Gly Tyr Asn Ile Gly Val Ile Asn Ala Pro  
344 35 40 45  
346 cag aag gtg att gaa cag agc tac aat gag acg tgg ctg ggg agg cag 192  
347 Gln Lys Val Ile Glu Gln Ser Tyr Asn Glu Thr Trp Leu Gly Arg Gln  
348 50 55 60  
350 ggg cct gag atc gat tat cct tat gat gtt cct gat tat gct gag gga 240  
351 Gly Pro Glu Ile Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Glu Gly  
352 65 70 75 80  
354 ccc agc tcc atc cct cca ggc acc ctc acc acc ctc tgg gcc ctc tcc 288  
355 Pro Ser Ser Ile Pro Pro Gly Thr Leu Thr Thr Leu Trp Ala Leu Ser  
356 85 90 95  
358 gtg gcc atc ttt tcc gtg ggc ggc atg att tcc tcc ttc ctc att ggt 336  
359 Val Ala Ile Phe Ser Val Gly Gly Met Ile Ser Ser Phe Leu Ile Gly  
360 100 105 110  
362 atc atc tct cag tgg ctt gga agg aaa agg gcc atg ctg gtc aac aat 384  
363 Ile Ile Ser Gln Trp Leu Gly Arg Lys Arg Ala Met Leu Val Asn Asn  
364 115 120 125  
366 gtc ctg gcg gtg ctg ggg ggc agc ctc atg ggc ctg gcc aac gct gct 432  
367 Val Leu Ala Val Leu Gly Gly Ser Leu Met Gly Leu Ala Asn Ala Ala  
368 130 135 140  
370 gcc tcc tat gaa atg ctc atc ctt gga cga ttc ctc att ggc gcc tac 480  
371 Ala Ser Tyr Glu Met Leu Ile Leu Gly Arg Phe Leu Ile Gly Ala Tyr  
372 145 150 155 160  
374 tca ggg ctg aca tca ggg ctg gtg ccc atg tac gtg ggg gag att gct 528  
375 Ser Gly Leu Thr Ser Gly Leu Val Pro Met Tyr Val Gly Glu Ile Ala  
376 165 170 175

RAW SEQUENCE LISTING ERROR SUMMARY                   DATE: 02/07/2007  
PATENT APPLICATION: US/10/567,894A               TIME: 11:41:58

*FYL*  
Input Set : N:\efs\02\_07\_07\10567894a\_efs\FBRIC54SeqList.txt  
Output Set: N:\CRF4\02072007\J567894A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:57; Xaa Pos. 227,436  
Seq#:58; Xaa Pos. 227,436

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/567,894A

DATE: 02/07/2007

TIME: 11:41:58

Input Set : N:\efs\02\_07\_07\10567894a\_efs\FBRIC54SeqList.txt  
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:7336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:789

M:341 Repeated in SeqNo=57

L:7562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:224

M:341 Repeated in SeqNo=58